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SEQUENCE LISTING

<110> Van der Geize, Robert
Hessels, Gerda
Dijkhuizen, Lubbert
Van der Meijden, Peter

<120> New expression system from Rhodococcus

<130> 2002.744US

<140> 10/537,201
<141> 2005-06-02

<150> PCT/EP03/050928
<151> 2003-12-02

<150> EP02080054.6
<151> 2002-12-03

<160> 13

<170> PatentIn Ver. 2.1

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<221> CDS

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ggc gga gcg ctg acc ggc gca tat acc gcc gct gct cag gga ttg acg 96
Gly Gly Ala Leu Thr Gly Ala Tyr Thr Ala Ala Ala Gln Gly Leu Thr
20 25 30
acg atc gtc ctc gag aaa acc gat cgt ttc ggc ggg acc tcc gcc tac 144
Thr Ile Val Leu Glu Lys Thr Asp Arg Phe Gly Gly Thr Ser Ala Tyr
35 40 45
tcg ggc gcc tcg atc tgg ctc cca ggt acc cag gtg cag gaa cgc gcc 192
Ser Gly Ala Ser Ile Trp Leu Pro Gly Thr Gln Val Gln Glu Arg Ala
50 55 60
gga ctt ccc gac tcg acc gag aat gcc cgc acc tat ctg cgc gcg ttg 240
Gly Leu Pro Asp Ser Thr Glu Asn Ala Arg Thr Tyr Leu Arg Ala Leu
65 70 75 80
ctc ggt gac gcc gag tcc gag cgc cag gac gcc tac gtc gag acc gct 288
Leu Gly Asp Ala Glu Ser Glu Arg Gln Asp Ala Tyr Val Glu Thr Ala
85 90 95
ccc gct gtc gtc gct cta ctc gag cag aac ccg aac atc gaa ttc gag 336
Pro Ala Val Val Ala Leu Leu Glu Gln Asn Pro Asn Ile Glu Phe Glu
100 105 110

ttc cgt gcg ttc ccc gac tac tac aaa gcc gaa ggc cg ^g atg gac acg Phe Arg Ala Phe Pro Asp Tyr Tyr Lys Ala Glu Gly Arg Met Asp Thr 115 120 125	384
gga cgc tcc atc aac cct ctc gat ctc gat ccc gcc gac atc ggt gac Gly Arg Ser Ile Asn Pro Leu Asp Leu Asp Pro Ala Asp Ile Gly Asp 130 135 140	432
ctc gcc ggc aag gtg cgt ccg gaa ctg gac caa gac cgc acc ggt cag Leu Ala Gly Lys Val Arg Pro Glu Leu Asp Gln Asp Arg Thr Gly Gln 145 150 155 160	480
gat cat gct ccc ggc ccg atg atc ggt ggg cgc gca ctg atc ggc cgt Asp His Ala Pro Gly Pro Met Ile Gly Gly Arg Ala Leu Ile Gly Arg 165 170 175	528
ctg ctg gcc gca gtt cag agc acc ggt aag gca gaa ctt cgc acc gaa Leu Leu Ala Ala Val Gln Ser Thr Gly Lys Ala Glu Leu Arg Thr Glu 180 185 190	576
tcc gtc ctc acc tcc ctg atc gtg gaa gac ggc cgt gtt gtc ggc gcc Ser Val Leu Thr Ser Leu Ile Val Glu Asp Gly Arg Val Val Gly Ala 195 200 205	624
gag gtc gaa tcc ggc ggc gaa acc cag cga atc aag gcg aac cgc ggt Glu Val Glu Ser Gly Gly Glu Thr Gln Arg Ile Lys Ala Asn Arg Gly 210 215 220	672
gtc ctg atg gca gca ggc ggc atc gaa ggc aac gcc gag atg cgt gag Val Leu Met Ala Ala Gly Gly Ile Glu Gly Asn Ala Glu Met Arg Glu 225 230 235 240	720
cag gca ggc acc ccc ggc aag gcg atc tgg agt atg ggt ccc ttc ggc Gln Ala Gly Thr Pro Gly Lys Ala Ile Trp Ser Met Gly Pro Phe Gly 245 250 255	768
gcc aac acc ggc gac gcg atc tct gcc ggt att gct gtc ggc ggc gca Ala Asn Thr Gly Asp Ala Ile Ser Ala Gly Ile Ala Val Gly Gly Ala 260 265 270	816
aca gcc ttg ctc gat cag gcg tgg ttc tgc ccc ggc gtc gag cag ccc Thr Ala Leu Leu Asp Gln Ala Trp Phe Cys Pro Gly Val Glu Gln Pro 275 280 285	864
gac ggc agc gcc gcc ttc atg gtc ggc gtt cgc ggt ggg ctc gtc gtc Asp Gly Ser Ala Ala Phe Met Val Gly Val Arg Gly Gly Leu Val Val 290 295 300	912
gac agc gcc ggt gag cgc tac ctc aac gag tcg ctt ccg tac gac cag Asp Ser Ala Gly Glu Arg Tyr Leu Asn Glu Ser Leu Pro Tyr Asp Gln 305 310 315 320	960
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tgc atc ccg aac acg gcg ccc gcc aag cac ctc gaa gcc gga acg tgg		1104	
Cys Ile Pro Asn Thr Ala Pro Ala Lys His Leu Glu Ala Gly Thr Trp			
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gtc ggt gcc gac act ctc gaa gaa ctc gct gcc aag acc gga cta ccg		1152	
Val Gly Ala Asp Thr Leu Glu Leu Ala Ala Lys Thr Gly Leu Pro			
370	375	380	
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Ala Asp Ala Leu Arg Ser Thr Val Glu Lys Phe Asn Asp Ala Ala Lys			
385	390	395	400
ctg ggc gtc gac gaa gag ttc cat cgc ggc gaa gac ccg tac gac gcg		1248	
Leu Gly Val Asp Glu Glu Phe His Arg Gly Glu Asp Pro Tyr Asp Ala			
405	410	415	
ttc ttc tgc cca ccc aac ggc ggt gcg aat gcg gca ctg acg gcc atc		1296	
Phe Phe Cys Pro Pro Asn Gly Gly Ala Asn Ala Ala Leu Thr Ala Ile			
420	425	430	
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Glu Asn Gly Pro Phe Tyr Ala Ala Arg Ile Val Leu Ser Asp Leu Gly			
435	440	445	
acc aag ggc gga ttg gtc acc gac gtc aac ggc cga gtc ctg cgt gct		1392	
Thr Lys Gly Gly Leu Val Thr Asp Val Asn Gly Arg Val Leu Arg Ala			
450	455	460	
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Asp Gly Ser Ala Ile Asp Gly Leu Tyr Ala Ala Gly Asn Thr Ser Ala			
465	470	475	480
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Ser Leu Ser Gly Arg Phe Tyr Pro Gly Pro Gly Val Pro Leu Gly Thr			
485	490	495	
gct atg gtc ttc tcg tac cga gca gct cag gac atg gcg aag taa		1533	
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<212> PRT
<213> Rhodococcus erythropolis

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Thr Ile Val Leu Glu Lys Thr Asp Arg Phe Gly Gly Thr Ser Ala Tyr			
35	40	45	
Ser Gly Ala Ser Ile Trp Leu Pro Gly Thr Gln Val Gln Glu Arg Ala			
50	55	60	

Gly Leu Pro Asp Ser Thr Glu Asn Ala Arg Thr Tyr Leu Arg Ala Leu
65 70 75 80

Leu Gly Asp Ala Glu Ser Glu Arg Gln Asp Ala Tyr Val Glu Thr Ala
85 90 95

Pro Ala Val Val Ala Leu Leu Glu Gln Asn Pro Asn Ile Glu Phe Glu
100 105 110

Phe Arg Ala Phe Pro Asp Tyr Tyr Lys Ala Glu Gly Arg Met Asp Thr
115 120 125

Gly Arg Ser Ile Asn Pro Leu Asp Leu Asp Pro Ala Asp Ile Gly Asp
130 135 140

Leu Ala Gly Lys Val Arg Pro Glu Leu Asp Gln Asp Arg Thr Gly Gln
145 150 155 160

Asp His Ala Pro Gly Pro Met Ile Gly Gly Arg Ala Leu Ile Gly Arg
165 170 175

Leu Leu Ala Ala Val Gln Ser Thr Gly Lys Ala Glu Leu Arg Thr Glu
180 185 190

Ser Val Leu Thr Ser Leu Ile Val Glu Asp Gly Arg Val Val Gly Ala
195 200 205

Glu Val Glu Ser Gly Gly Glu Thr Gln Arg Ile Lys Ala Asn Arg Gly
210 215 220

Val Leu Met Ala Ala Gly Gly Ile Glu Gly Asn Ala Glu Met Arg Glu
225 230 235 240

Gln Ala Gly Thr Pro Gly Lys Ala Ile Trp Ser Met Gly Pro Phe Gly
245 250 255

Ala Asn Thr Gly Asp Ala Ile Ser Ala Gly Ile Ala Val Gly Gly Ala
260 265 270

Thr Ala Leu Leu Asp Gln Ala Trp Phe Cys Pro Gly Val Glu Gln Pro
275 280 285

Asp Gly Ser Ala Ala Phe Met Val Gly Val Arg Gly Gly Leu Val Val
290 295 300

Asp Ser Ala Gly Glu Arg Tyr Leu Asn Glu Ser Leu Pro Tyr Asp Gln
305 310 315 320

Phe Gly Arg Ala Met Asp Ala His Asp Asp Asn Gly Ser Ala Val Pro
325 330 335

Ser Phe Met Ile Phe Asp Ser Arg Glu Gly Gly Leu Pro Ala Ile
340 345 350

Cys Ile Pro Asn Thr Ala Pro Ala Lys His Leu Glu Ala Gly Thr Trp
355 360 365

Val Gly Ala Asp Thr Leu Glu Glu Leu Ala Ala Lys Thr Gly Leu Pro
370 375 380

Ala Asp Ala Leu Arg Ser Thr Val Glu Lys Phe Asn Asp Ala Ala Lys

385	390	395	400
Leu Gly Val Asp Glu Glu Phe His Arg Gly Glu Asp Pro Tyr Asp Ala			
405	410	415	
Phe Phe Cys Pro Pro Asn Gly Gly Ala Asn Ala Ala Leu Thr Ala Ile			
420	425	430	
Glu Asn Gly Pro Phe Tyr Ala Ala Arg Ile Val Leu Ser Asp Leu Gly			
435	440	445	
Thr Lys Gly Gly Leu Val Thr Asp Val Asn Gly Arg Val Leu Arg Ala			
450	455	460	
Asp Gly Ser Ala Ile Asp Gly Leu Tyr Ala Ala Gly Asn Thr Ser Ala			
465	470	475	480
Ser Leu Ser Gly Arg Phe Tyr Pro Gly Pro Gly Val Pro Leu Gly Thr			
485	490	495	
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<213> Rhodococcus erythropolis

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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

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<213> Rhodococcus erythropolis

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<222> (1)..(624)

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Pro Ser Ser Asp Glu Gln Arg Ala Arg His Val Arg Met Leu Glu Ala	
20 25 30	
gc ^c gc ^c gaa tt ^g gg ^g acc gag aaa gaa ct ^c tca cg ^g gt ^t ca ^g at ^g ca ^c	144
Ala Ala Glu Leu Gly Thr Glu Lys Glu Leu Ser Arg Val Gln Met His	
35 40 45	
ga ^a gt ^t gc ^c aag cg ^g gc ^a gg ^c gt ^g gc ^c at ^c ct ^c ta ^c cg ^c ta ^t	192
Glu Val Ala Lys Arg Ala Gly Val Ala Ile Gly Thr Leu Tyr Arg Tyr	
50 55 60	
tt ^c ct ^c tc ^g aag ac ^g ca ^c ct ^c tt ^c gt ^c gct gt ^g at ^g gt ^c ga ^g ca ^t	240
Phe Pro Ser Lys Thr His Leu Phe Val Ala Val Met Val Glu Gln Ile	
65 70 75 80	
ga ^t ca ^g at ^c gg ^c ga ^c ag ^t tt ^c gc ^c aag ca ^t ca ^g gt ^g ca ^g tc ^g gc ^c aa ^t	288
Asp Gln Ile Gly Asp Ser Phe Ala Lys His Gln Val Gln Ser Ala Asn	
85 90 95	
cc ^g ca ^g ga ^c gc ^c gt ^g ta ^c ga ^g gt ^c ct ^g gt ^g cg ^c gc ^g ac ^t cg ^c gg ^g tt ^a	336
Pro Gln Asp Ala Val Tyr Glu Val Leu Val Arg Ala Thr Arg Gly Leu	
100 105 110	
ct ^g cg ^t cg ^g gc ^c ct ^t tc ^g ac ^t gc ^g at ^g ct ^g ca ^g tc ^g tc ^c ag ^t ac ^c	384
Leu Arg Arg Pro Ala Leu Ser Thr Ala Met Leu Gln Ser Ser Ser Thr	
115 120 125	
gc ^c aa ^c gt ^c gc ^g ac ^g gt ^g cc ^g ga ^c gt ^g gg ^c aag at ^c ga ^t cg ^c gg ^c tt ^c	432
Ala Asn Val Ala Thr Val Pro Asp Val Gly Lys Ile Asp Arg Gly Phe	
130 135 140	
cg ^g ca ^g at ^c at ^c ct ^c ga ^t gc ^g gg ^g at ^c ga ^g aa ^c cc ^g ac ^c ga ^g gaa	480
Arg Gln Ile Ile Leu Asp Ala Ala Gly Ile Glu Asn Pro Thr Glu Glu	
145 150 155 160	
ga ^c aa ^c cc ^g tt ^t cg ^t ct ^g at ^g ca ^g ct ^g tg ^g tt ^c gg ^g gt ^c at ^c	528
Asp Asn Thr Gly Leu Arg Leu Leu Met Gln Leu Trp Phe Gly Val Ile	
165 170 175	
ca ^a tc ^g tg ^c ct ^c aa ^c gg ^t cg ^a att tcc at ^c cc ^g ga ^t gc ^g ga ^g ta ^c ga ^c	576
Gln Ser Cys Leu Asn Gly Arg Ile Ser Ile Pro Asp Ala Glu Tyr Asp	
180 185 190	
at ^c cg ^c aag gg ^g tg ^c ga ^c ct ^t ct ^g gt ^g aat ct ^c tca cg ^a ca ^c tg ^a	624
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195 200 205	

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<213> Rhodococcus erythropolis

<400> 6

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35	40	45
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50	55	60
Phe Pro Ser Lys Thr His Leu Phe Val Ala Val Met Val Glu Gln Ile		
65	70	75
Asp Gln Ile Gly Asp Ser Phe Ala Lys His Gln Val Gln Ser Ala Asn		
85	90	95
Pro Gln Asp Ala Val Tyr Glu Val Leu Val Arg Ala Thr Arg Gly Leu		
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Ala Asn Val Ala Thr Val Pro Asp Val Gly Lys Ile Asp Arg Gly Phe		
130	135	140
Arg Gln Ile Ile Leu Asp Ala Ala Gly Ile Glu Asn Pro Thr Glu Glu		
145	150	155
Asp Asn Thr Gly Leu Arg Leu Leu Met Gln Leu Trp Phe Gly Val Ile		
165	170	175
Gln Ser Cys Leu Asn Gly Arg Ile Ser Ile Pro Asp Ala Glu Tyr Asp		
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<220>
 <223> Description of Artificial Sequence:primer

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<220>
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<210> 11
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SEQUENCE LISTING

<110> Van der Geize, Robert
Hessels, Gerda
Dijkhuizen, Lubbert
Van der Meijden, Peter

<120> New expression system from Rhodococcus

<130> 2002.744US

<140> 10/537,201
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<170> PatentIn Ver. 2.1

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Gly Gly Ala Leu Thr Gly Ala Tyr Thr Ala Ala Ala Gln Gly Leu Thr
20 25 30

acg atc gtc ctc gag aaa acc gat cgt ttc ggc ggg acc tcc gcc tac 144
Thr Ile Val Leu Glu Lys Thr Asp Arg Phe Gly Gly Thr Ser Ala Tyr
35 40 45

tcg ggc gcc tcg atc tgg ctc cca ggt acc cag gtg cag gaa cgc gcc 192
Ser Gly Ala Ser Ile Trp Leu Pro Gly Thr Gln Val Gln Glu Arg Ala
50 55 60

gga ctt ccc gac tcg acc gag aat gcc cgc acc tat ctg cgc gcg ttg 240
Gly Leu Pro Asp Ser Thr Glu Asn Ala Arg Thr Tyr Leu Arg Ala Leu
65 70 75 80

ctc ggt gac gcc gag tcc gag cgc cag gac gcc tac gtc gag acc gct 288
Leu Gly Asp Ala Glu Ser Glu Arg Gln Asp Ala Tyr Val Glu Thr Ala
85 90 95

ccc gct gtc gtc gct cta ctc gag cag aac ccg aac atc gaa ttc gag 336
Pro Ala Val Val Ala Leu Leu Glu Gln Asn Pro Asn Ile Glu Phe Glu
100 105 110

ttc cgt gcg ttc ccc gac tac tac aaa gcc gaa ggc cog atg gac acg		384	
Phe Arg Ala Phe Pro Asp Tyr Tyr Lys Ala Glu Gly Arg Met Asp Thr			
115	120	125	
gga cgc tcc atc aac cct ctc gat ctc gat ccc gcc gac atc ggt gac		432	
Gly Arg Ser Ile Asn Pro Leu Asp Leu Asp Pro Ala Asp Ile Gly Asp			
130	135	140	
ctc gcc ggc aag gtg cgt ccg gaa ctg gac caa gac cgc acc ggt cag		480	
Leu Ala Gly Lys Val Arg Pro Glu Leu Asp Gln Asp Arg Thr Gly Gln			
145	150	155	160
gat cat gct ccc ggc ccg atg atc ggt ggg cgc gca ctg atc ggc cgt		528	
Asp His Ala Pro Gly Pro Met Ile Gly Gly Arg Ala Leu Ile Gly Arg			
165	170	175	
ctg ctg gcc gca gtt cag agc acc ggt aag gca gaa ctt cgc acc gaa		576	
Leu Leu Ala Ala Val Gln Ser Thr Gly Lys Ala Glu Leu Arg Thr Glu			
180	185	190	
tcc gtc ctc acc tcc ctg atc gtg gaa gac ggc cgt gtt gtc ggc gcc		624	
Ser Val Leu Thr Ser Leu Ile Val Glu Asp Gly Arg Val Val Gly Ala			
195	200	205	
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210	215	220	
gtc ctg atg gca gca ggc ggc atc gaa ggc aac gcc gag atg cgt gag		720	
Val Leu Met Ala Ala Gly Gly Ile Glu Gly Asn Ala Glu Met Arg Glu			
225	230	235	240
cag gca ggc acc ccc ggc aag gcg atc tgg agt atg ggt ccc ttc ggc		768	
Gln Ala Gly Thr Pro Gly Lys Ala Ile Trp Ser Met Gly Pro Phe Gly			
245	250	255	
gcc aac acc ggc gac gcg atc tct gcc ggt att gct gtc ggc ggc gca		816	
Ala Asn Thr Gly Asp Ala Ile Ser Ala Gly Ile Ala Val Gly Gly Ala			
260	265	270	
aca gcc ttg ctc gat cag gcg tgg ttc tgc ccc ggc gtc gag cag ccc		864	
Thr Ala Leu Leu Asp Gln Ala Trp Phe Cys Pro Gly Val Glu Gln Pro			
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305	310	315	320
ttc gga cga gcc atg gat gct cac gac aac ggt tct gcc gtg ccg		1008	
Phe Gly Arg Ala Met Asp Ala His Asp Asp Asn Gly Ser Ala Val Pro			
325	330	335	
tcg ttc atg atc ttc gac tcg cgc gag ggt ggc gga ctg ccc gcc atc		1056	
Ser Phe Met Ile Phe Asp Ser Arg Glu Gly Gly Leu Pro Ala Ile			
340	345	350	

tgc atc ccg aac acg gcg ccc gcc aag cac ctc gaa gcc gga acg tgg		1104	
Cys Ile Pro Asn Thr Ala Pro Ala Lys His Leu Glu Ala Gly Thr Trp			
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gtc ggt gcc gac act ctc gaa gaa ctc gct gcc aag acc gga cta ccg		1152	
Val Gly Ala Asp Thr Leu Glu Leu Ala Ala Lys Thr Gly Leu Pro			
370	375	380	
gcc gac gca ttg cgc agc act gtc gaa aag ttc aac gat gcc gca aaa		1200	
Ala Asp Ala Leu Arg Ser Thr Val Glu Lys Phe Asn Asp Ala Ala Lys			
385	390	395	400
ctg ggc gtc gac gaa gag ttc cat cgc ggc gaa gac ccg tac gac gcg		1248	
Leu Gly Val Asp Glu Glu Phe His Arg Gly Glu Asp Pro Tyr Asp Ala			
405	410	415	
ttc ttc tgc cca ccc aac ggc ggt gcg aat gcg gca ctg acg gcc atc		1296	
Phe Phe Cys Pro Pro Asn Gly Gly Ala Asn Ala Ala Leu Thr Ala Ile			
420	425	430	
gag aac gga ccg ttc tac gcg gcc cgc atc gtc ctc agt gac ctc ggc		1344	
Glu Asn Gly Pro Phe Tyr Ala Ala Arg Ile Val Leu Ser Asp Leu Gly			
435	440	445	
acc aag ggc gga ttg gtc acc gac gtc aac ggc cga gtc ctg cgt gct		1392	
Thr Lys Gly Gly Leu Val Thr Asp Val Asn Gly Arg Val Leu Arg Ala			
450	455	460	
gac ggc agc gcc atc gac ggc ctg tac gcc gcc ggc aac acg agc gcg		1440	
Asp Gly Ser Ala Ile Asp Gly Leu Tyr Ala Ala Gly Asn Thr Ser Ala			
465	470	475	480
tca ctg agc ggc cgc ttc tac ccc ggc ccc gga gtt cca ctc ggc acg		1488	
Ser Leu Ser Gly Arg Phe Tyr Pro Gly Pro Gly Val Pro Leu Gly Thr			
485	490	495	
gct atg gtc ttc tcg tac cga gca gct cag gac atg gcg aag taa		1533	
Ala Met Val Phe Ser Tyr Arg Ala Ala Gln Asp Met Ala Lys			
500	505	510	
cgcatcaa		1543	

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<212> PRT
<213> Rhodococcus erythropolis

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Met Gln Asp Trp Thr Ser Glu Cys Asp Val Leu Val Val Gly Ser Gly			
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Gly Gly Ala Leu Thr Gly Ala Tyr Thr Ala Ala Gln Gly Leu Thr			
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Thr Ile Val Leu Glu Lys Thr Asp Arg Phe Gly Gly Thr Ser Ala Tyr			
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Ser Gly Ala Ser Ile Trp Leu Pro Gly Thr Gln Val Gln Glu Arg Ala			
50	55	60	

Gly Leu Pro Asp Ser Thr Glu Asn Ala Arg Thr Tyr Leu Arg Ala Leu
65 70 75 80

Leu Gly Asp Ala Glu Ser Glu Arg Gln Asp Ala Tyr Val Glu Thr Ala
85 90 95

Pro Ala Val Val Ala Leu Leu Glu Gln Asn Pro Asn Ile Glu Phe Glu
100 105 110

Phe Arg Ala Phe Pro Asp Tyr Tyr Lys Ala Glu Gly Arg Met Asp Thr
115 120 125

Gly Arg Ser Ile Asn Pro Leu Asp Leu Asp Pro Ala Asp Ile Gly Asp
130 135 140

Leu Ala Gly Lys Val Arg Pro Glu Leu Asp Gln Asp Arg Thr Gly Gln
145 150 155 160

Asp His Ala Pro Gly Pro Met Ile Gly Gly Arg Ala Leu Ile Gly Arg
165 170 175

Leu Leu Ala Ala Val Gln Ser Thr Gly Lys Ala Glu Leu Arg Thr Glu
180 185 190

Ser Val Leu Thr Ser Leu Ile Val Glu Asp Gly Arg Val Val Gly Ala
195 200 205

Glu Val Glu Ser Gly Gly Glu Thr Gln Arg Ile Lys Ala Asn Arg Gly
210 215 220

Val Leu Met Ala Ala Gly Gly Ile Glu Gly Asn Ala Glu Met Arg Glu
225 230 235 240

Gln Ala Gly Thr Pro Gly Lys Ala Ile Trp Ser Met Gly Pro Phe Gly
245 250 255

Ala Asn Thr Gly Asp Ala Ile Ser Ala Gly Ile Ala Val Gly Gly Ala
260 265 270

Thr Ala Leu Leu Asp Gln Ala Trp Phe Cys Pro Gly Val Glu Gln Pro
275 280 285

Asp Gly Ser Ala Ala Phe Met Val Gly Val Arg Gly Gly Leu Val Val
290 295 300

Asp Ser Ala Gly Glu Arg Tyr Leu Asn Glu Ser Leu Pro Tyr Asp Gln
305 310 315 320

Phe Gly Arg Ala Met Asp Ala His Asp Asp Asn Gly Ser Ala Val Pro
325 330 335

Ser Phe Met Ile Phe Asp Ser Arg Glu Gly Gly Leu Pro Ala Ile
340 345 350

Cys Ile Pro Asn Thr Ala Pro Ala Lys His Leu Glu Ala Gly Thr Trp
355 360 365

Val Gly Ala Asp Thr Leu Glu Glu Leu Ala Ala Lys Thr Gly Leu Pro
370 375 380

Ala Asp Ala Leu Arg Ser Thr Val Glu Lys Phe Asn Asp Ala Ala Lys

385	390	395	400
Leu Gly Val Asp Glu Glu Phe His Arg Gly Glu Asp Pro Tyr Asp Ala			
405	410	415	
Phe Phe Cys Pro Pro Asn Gly Gly Ala Asn Ala Ala Leu Thr Ala Ile			
420	425	430	
Glu Asn Gly Pro Phe Tyr Ala Ala Arg Ile Val Leu Ser Asp Leu Gly			
435	440	445	
Thr Lys Gly Gly Leu Val Thr Asp Val Asn Gly Arg Val Leu Arg Ala			
450	455	460	
Asp Gly Ser Ala Ile Asp Gly Leu Tyr Ala Ala Gly Asn Thr Ser Ala			
465	470	475	480
Ser Leu Ser Gly Arg Phe Tyr Pro Gly Pro Gly Val Pro Leu Gly Thr			
485	490	495	
Ala Met Val Phe Ser Tyr Arg Ala Ala Gln Asp Met Ala Lys			
500	505	510	

<210> 3
<211> 158
<212> DNA
<213> Rhodococcus erythropolis

<400> 3
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atctcggcat attgcccgt cagtggacc tggcatggcc ttccagtgcc gtgcggatt 120
ccgtggacac cccaccctct tggagtaagg acgcaatg 158

<210> 4
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 4
ggcgacgtt ccgagaatt 19

<210> 5
<211> 624
<212> DNA
<213> Rhodococcus erythropolis

<220>
<221> CDS
<222> (1)..(624)

<400> 5
atg ggg gcg acg ttg ccg aga att gcc gag gtc agg gac gct gct gag 48
Met Gly Ala Thr Leu Pro Arg Ile Ala Glu Val Arg Asp Ala Ala Glu

1

5

10

15

ccc agt tcg gac gag cag cg ^g gc ^g cg ^c cat gt ^g cg ^g at ^g ct ^g gaa gc ^g	96
Pro Ser Ser Asp Glu Gln Arg Ala Arg His Val Arg Met Leu Glu Ala	
20 25 30	
gc ^c gc ^c gaa tt ^g gg ^g acc gag aaa gaa ct ^c tca cg ^g gt ^t ca ^g at ^g ca ^c	144
Ala Ala Glu Leu Gly Thr Glu Lys Glu Leu Ser Arg Val Gln Met His	
35 40 45	
gaa gtt gc ^c aag cg ^g gc ^a gg ^c gt ^g gc ^c at ^c ct ^c ta ^c cg ^c ta ^t	192
Glu Val Ala Lys Arg Ala Gly Val Ala Ile Gly Thr Leu Tyr Arg Tyr	
50 55 60	
ttc cct tc ^g aag ac ^g ca ^c ct ^c tc ^t gt ^c g ^c at ^t ct ^c ta ^c cg ^c ta ^t	240
Phe Pro Ser Lys Thr His Leu Phe Val Ala Val Met Val Glu Gln Ile	
65 70 75 80	
gat ca ^g at ^c gg ^c ga ^c ag ^t tt ^c gc ^c a ^a g ^a ca ^g gt ^g ca ^g tc ^g gc ^c aa ^t	288
Asp Gln Ile Gly Asp Ser Phe Ala Lys His Gln Val Gln Ser Ala Asn	
85 90 95	
cc ^g ca ^g ga ^c gg ^c gt ^g ta ^c ga ^g gt ^c ct ^g cg ^c gc ^g ac ^t cg ^c gg ^g tt ^a	336
Pro Gln Asp Ala Val Tyr Glu Val Leu Val Arg Ala Thr Arg Gly Leu	
100 105 110	
ct ^g cg ^t cg ^g gc ^c ct ^t tc ^g ac ^t gc ^g at ^g ct ^g ca ^g tc ^g tc ^c ag ^t ac ^c	384
Leu Arg Arg Pro Ala Leu Ser Thr Ala Met Leu Gln Ser Ser Ser Thr	
115 120 125	
gc ^c aa ^c gt ^c gc ^g ac ^g gt ^g cc ^g ga ^c gt ^g gg ^c aa ^a at ^c ga ^t cg ^c gg ^c tt ^a	432
Ala Asn Val Ala Thr Val Pro Asp Val Gly Lys Ile Asp Arg Gly Phe	
130 135 140	
cg ^g ca ^g at ^c at ^c ct ^c ga ^t gc ^c gg ^g at ^c ga ^g aa ^c cc ^g ac ^c ga ^g gaa	480
Arg Gln Ile Ile Leu Asp Ala Ala Gly Ile Glu Asn Pro Thr Glu Glu	
145 150 155 160	
ga ^c aa ^a cc ^g tt ^g cg ^t ct ^g at ^g ca ^g ct ^g tg ^g tt ^c gg ^g gt ^c at ^c	528
Asp Asn Thr Gly Leu Arg Leu Leu Met Gln Leu Trp Phe Gly Val Ile	
165 170 175	
ca ^a tc ^g tg ^c ct ^c aa ^c gg ^t cg ^a att tcc at ^c cc ^g ga ^t gc ^g ga ^g ta ^c ga ^c	576
Gln Ser Cys Leu Asn Gly Arg Ile Ser Ile Pro Asp Ala Glu Tyr Asp	
180 185 190	
at ^c cg ^c a ^a gg ^g tg ^c ga ^c ct ^c ct ^t ct ^g gt ^g aa ^t ct ^c tca cg ^a ca ^c tg ^a	624
Ile Arg Lys Gly Cys Asp Leu Leu Leu Val Asn Leu Ser Arg His	
195 200 205	

<210> 6

<211> 207

<212> PRT

<213> Rhodococcus erythropolis

<400> 6

Met Gly Ala Thr Leu Pro Arg Ile Ala Glu Val Arg Asp Ala Ala Glu	
1 5 10 15	

Pro Ser Ser Asp Glu Gln Arg Ala Arg His Val Arg Met Leu Glu Ala

20

25

30

Ala Ala Glu Leu Gly Thr Glu Lys Glu Leu Ser Arg Val Gln Met His
35 40 45

Glu Val Ala Lys Arg Ala Gly Val Ala Ile Gly Thr Leu Tyr Arg Tyr
50 55 60

Phe Pro Ser Lys Thr His Leu Phe Val Ala Val Met Val Glu Gln Ile
65 70 75 80

Asp Gln Ile Gly Asp Ser Phe Ala Lys His Gln Val Gln Ser Ala Asn
85 90 95

Pro Gln Asp Ala Val Tyr Glu Val Leu Val Arg Ala Thr Arg Gly Leu
100 105 110

Leu Arg Arg Pro Ala Leu Ser Thr Ala Met Leu Gln Ser Ser Ser Thr
115 120 125

Ala Asn Val Ala Thr Val Pro Asp Val Gly Lys Ile Asp Arg Gly Phe
130 135 140

Arg Gln Ile Ile Leu Asp Ala Ala Gly Ile Glu Asn Pro Thr Glu Glu
145 150 155 160

Asp Asn Thr Gly Leu Arg Leu Leu Met Gln Leu Trp Phe Gly Val Ile
165 170 175

Gln Ser Cys Leu Asn Gly Arg Ile Ser Ile Pro Asp Ala Glu Tyr Asp
180 185 190

Ile Arg Lys Gly Cys Asp Leu Leu Leu Val Asn Leu Ser Arg His
195 200 205

<210> 7
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 7
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<210> 8
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 8
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<210> 9

<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 9
ataggtacca tatgtgcgtc cttactccaa gaggg 35

<210> 10
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 10
gcgcatatgg ctaagaatca ggcaccc 27

<210> 11
<211> 30
<212> DNA
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<220>
<223> Description of Artificial Sequence:primer

<400> 11
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<210> 12
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 12
ggccatatgt tgaccacaga cgtgacgacc 30

<210> 13
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 13
gccactagtt cactgcgtc ctcctgcacg 30